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Software *PowerTools* for Genetic Analysis

Contact Information:
John Fosnacht
SoftGenetics LLC
The Oakwood Centre
Suite 350
State College PA 16803

FOR IMMEDIATE RELEASE

New Stepwise Paired End assembler for MiSeq data

January 11, 2012, State College PA SoftGenetics announced the availability of a new assembly tool for Illumina MiSeq platform paired end sequencing reads. The new assembler, available in the company's NextGENe software, resolves repeat region assembly problems typical of short reads sequencing. The new assembly tool is most well suited for the assembly of smaller genomes from short reads generated by the Illumina MiSeq platform.

NextGENe software resolves this problem with a stepwise paired-end assembly methodology, indicated Megan Manion, NextGENe Technical Product Manager. "Typically the end of a contig produced by assembly may indicate a repeat region. To resolve this the software first calls in the reads paired to those assembled (using overlaps) at the end of the contig, up to 1 ½ times the library size from the end. These reads are then assembled and the software chooses the most complete assembly to continue the contig. Shorter assemblies are not used because they are formed by repetitive sequences erroneously assembled together due to their similarity. This results in a highly accurate and efficient tool for assembly of paired-end or mate-pair data. A small bacterial genome such as E. coli can be assembled into less than 70 contigs from a single MiSeq data run in less than 2 hours. The assembler can be run on relatively low-cost Windows® hardware- in this case the program needed less than 8 GB of RAM."

The company offers 30-day trials and no cost web-based training on its genetic analysis software packages Interested parties may request the software on the company website: www.softgenetics.com or via email: info@softgenetics.com.

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SoftGenetics, LLC specializes in the development of genetic analysis tools for both research and diagnostic applications. Hallmarks of SoftGenetics software tools are advanced technologies, providing exceptional accuracy, and sensitivity in an easy-to use Windows® user interface.